

09/830144

1/25

JCOS 3/d PCT/PTO

20 APR 2001

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Method for screening compounds inhibiting signal  
transduction through inflammatory cytokines

<130> C1-005PCT

<140>

<141>

<150> JP 1998-299962

<151> 1998-10-21

<160> 10

<170> PatentIn version 2.0

<210> 1

<211> 2656

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)..(1919)

<400> 1

gtcgagatcc atttgtctct aaagacggct gtggccgctg cctctacccc cgccacggat 60

cgcgggttag taggactgcg cggctccagg ctgagggtcg gtccggaggc gggtggcgc 120

gggtctcacc cggattgtcc gggtggcacc gttccggcc ccaccggcg ccgcgaggga 180

tc atg tct aca gcc tct gcc tcc tcc tcc tcg tct tcg gcc 227

Met Ser Thr Ala Ser Ala Ala Ser Ser Ser Ser Ser Ser Ala

1

5

10

15

ggt gag atg atc gaa gcc cct tcc cag gtc ctc aac ttt gaa gag atc 275

Gly Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile

20

25

30

gac tac aag gag atc gag gtg gaa gag gtt gtt gga aga gga gcc ttt 323

Asp Tyr Lys Glu Ile Glu Val Glu Val Val Gly Arg Gly Ala Phe

35

40

45

gga gtt gtt tgc aaa gct aag tgg aga gca aaa gat gtt gct att aaa 371

Gly Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys

50

55

60

caa ata gaa agt gaa tct gag agg aaa gcg ttt att gta gag ctt cg 419

Gln Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg

65

70

75

cag tta tcc cgt gtg aac cat cct aat att gta aag ctt tat gga gcc 467

Gln Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala

80

85

90

95

tgc ttg aat cca gtg tgt ctt gtg atg gaa tat gct gaa ggg ggc tct 515

Cys Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Ser

100

105

110

tta tat aat gtg ctg cat ggt gct gaa cca ttg cca tat tat act gct 563

Leu Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala

115

120

125

gcc cac gca atg agt tgg tgt tta cag tgt tcc caa gga gtg gct tat 611

Ala His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr

130

135

140

ctt cac agc atg caa ccc aaa gcg cta att cac agg gac ctg aaa cca 659

Leu His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro

145	150	155	
<pre>cca aac tta ctg ctg gtt gca ggg ggg aca gtt cta aaa att tgt gat      707 Pro Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp</pre>			
160	165	170	175
<pre>ttt ggt aca gcc tgt gac att cag aca cac atg acc aat aac aag ggg      755 Phe Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly</pre>			
180	185	190	
<pre>agt gct gct tgg atg gca cct gaa gtt ttt gaa ggt agt aat tac agt      803 Ser Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser</pre>			
195	200	205	
<pre>gaa aaa tgt gac gtc ttc agc tgg ggt att att ctt tgg gaa gtg ata      851 Glu Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile</pre>			
210	215	220	
<pre>acg cgt cgg aaa ccc ttt gat gag att ggt ggc cca gct ttc cga atc      899 Thr Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile</pre>			
225	230	235	
<pre>atg tgg gct gtt cat aat ggt act cga cca cca ctg ata aaa aat tta      947 Met Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu</pre>			
240	245	250	255

cct aag ccc att gag agc ctg atg act cgt tgt tgg tct aaa gat cct 995

Pro Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro

260

265

270

tcc cag cgc cct tca atg gag gaa att gtg aaa ata atg act cac ttg 1043

Ser Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu

275

280

285

atg cgg tac ttt cca gga gca gat gag cca tta cag tat cct tgt cag 1091

Met Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln

290

295

300

tat tca gat gaa gga cag agc aac tct gcc acc agt aca ggc tca ttc 1139

Tyr Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe

305

310

315

atg gac att gct tct aca aat acg agt aac aaa agt gac act aat atg 1187

Met Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met

320

325

330

335

gag caa gtt cct gcc aca aat gat act att aag cgc tta gaa tca aaa 1235

Glu Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys

340

345

350

ttg ttg aaa aat cag gca aag caa cag agt gaa tct gga cgt tta agc 1283

Leu Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser

355

360

365

ttg gga gcc tcc cat ggg agc agt gtg gag agc ttg ccc cca acc tct 1331

Leu Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser

370

375

380

gag ggc aag agg atg agt gct gac atg tct gaa ata gaa gct agg atc 1379

Glu Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile

385

390

395

gcc gca acc aca ggc aac gga cag cca aga cgt aga tcc atc caa gac 1427

Ala Ala Thr Thr Gly Asn Gly Gln Pro Arg Arg Arg Ser Ile Gln Asp

400

405

410

415

ttg act gta act gga aca gaa cct ggt cag gtg agc agt agg tca tcc 1475

Leu Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser

420

425

430

agt ccc agt gtc aga atg att act acc tca gga cca acc tca gaa aag 1523

Ser Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Ser Glu Lys

435

440

445

cca act cga agt cat cca tgg acc cct gat gat tcc aca gat acc aat 1571

Pro Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn

450

455

460

gga tca gat aac tcc atc cca atg gct tat ctt aca ctg gat cac caa 1619

Gly Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln

465

470

475

cta cag cct cta gca ccg tgc cca aac tcc aaa gaa tct atg gca gtg 1667

Leu Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val

480

485

490

495

ttt gaa cag cat tgt aaa atg gca caa gaa tat atg aaa gtt caa aca 1715

Phe Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr

500

505

510

gaa att gca ttg tta tta cag aga aag caa gaa cta gtt gca gaa ctg 1763

Glu Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu

515

520

525

gac cag gat gaa aag gac cag caa aat aca tct cgc ctg gta cag gaa 1811

Asp Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu

530

535

540

cat aaa aag ctt tta gat gaa aac aaa agc ctt tct act tac tac cag 1859

His Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln

545

550

555

caa tgc aaa aaa caa cta gag gtc atc aga agt cag cag aaa cga 1907

Gln Cys Lys Lys Gln Leu Glu Val Ile Arg Ser Gln Gln Lys Arg

560

565

570

575

caa ggc act tca tgattctctg ggaccgttac attttgaat atgcaaagaa 1959

Gln Gly Thr Ser

agactttttt tttaaggaaaa ggaaaacctt ataatgacga ttcatgagtg tttagctttt 2019

ggcgtgttct gaatgccaac tgccatatatt tgctgcattt ttttcattgt ttatttcct 2079

tttctcatgg tggacataca attttactgt ttcattgcat aacatggtag catctgtgac 2139

ttgaatgagc agcactttgc aacttcaaaa cagatgcagt gaactgtggc tgtatatgca 2199

tgctcattgt gtgaaggcta gcctaacaga acaggaggt tcaaacttagc tgctatgtgc 2259

aaacagcgtc catttttca tattagaggt ggaacctcaa gaatgacttt attctgtat 2319

ctcatctcaa aatattaata attttttcc caaaagatgg tatataccaa gttaaagaca 2379

gggtattata aattagagt gattgggttgt atattacgga aatacggaac cttagggat 2439

agttccgtgt aaggccttg atgccagcat cttggatca gtactgaact cagttccatc 2499

cgtaaaatat gtaaaggtaa gtggcagctg ctctattaa taaaaggcagt ttaccggat 2559

ttttagac taaaatttga ttgtgataca ttgaacaaaa tgaaactcat ttttttaag 2619

gagtaaagat tttctttaga gcacaatgga tctcgac 2656

<210> 2

<211> 579

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Thr Ala Ser Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly

1 5 10 15

Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile Asp

20 25 30

Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe Gly

35 40 45

Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys Gln

50 55 60

Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg Gln

65 70 75 80

Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala Cys

85 90 95

Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser Leu

100 105 110

Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala Ala

115 120 125

His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr Leu

130 135 140

His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro Pro

145 150 155 160

Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp Phe

165 170 175

Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly Ser

180 185 190

Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser Glu

195 200 205

Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile Thr

210 215 220

Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile Met  
225 230 235 240

Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu Pro  
245 250 255

Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro Ser  
260 265 270

Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu Met  
275 280 285

Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln Tyr  
290 295 300

Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe Met  
305 310 315 320

Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met Glu  
325 330 335

Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys Leu  
340 345 350

Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser Leu

355

360

365

Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser Glu

370

375

380

Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile Ala

385

390

395

400

Ala Thr Thr Gly Asn Gly Gln Pro Arg Arg Arg Ser Ile Gln Asp Leu

405

410

415

Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser Ser

420

425

430

Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Ser Glu Lys Pro

435

440

445

Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn Gly

450

455

460

Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln Leu

465

470

475

480

Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val Phe

485

490

495

Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr Glu  
500 505 510

Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu Asp  
515 520 525

Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu His  
530 535 540

Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln Gln  
545 550 555 560

Cys Lys Lys Gln Leu Glu Val Ile Arg Ser Gln Gln Gln Lys Arg Gln  
565 570 575

Gly Thr Ser

<210> 3

<211> 1560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

&lt;222&gt; (30)..(1541)

&lt;400&gt; 3

gaattcgtgg cccgcagggt tcctccaag atg gcg gcg cag agg agg agc ttg 53

Met Ala Ala Gln Arg Arg Ser Leu

5

ctg cag agt gag cag cag cca agc tgg aca gat gac ctg cct ctc tgc 101

Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys

10

15

20

cac ctc tct ggg gtt ggc tca gcc tcc aac cgc agc tac tct gct gat 149

His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp

25

30

35

40

ggc aag ggc act gag agc cac ccg cca gag gac agc tgg ctc aag ttc 197

Gly Lys Gly Thr Glu Ser His Pro Pro Glu Asp Ser Trp Leu Lys Phe

45

50

55

agg agt gag aac aac tgc ttc ctg tat ggg gtc ttc aac ggc tat gat 245

Arg Ser Glu Asn Asn Cys Phe Leu Tyr Gly Val Phe Asn Gly Tyr Asp

60

65

70

ggc aac cga gtg acc aac ttc gtg gcc cag cgg ctg tcc gca gag ctc 293

Gly Asn Arg Val Thr Asn Phe Val Ala Gln Arg Leu Ser Ala Glu Leu

75

80

85

ctg ctg ggc cag ctg aat gcc gag cac gcc gag gcc gat gtg cgg cgt	341		
Leu Leu Gly Gln Leu Asn Ala Glu His Ala Glu Ala Asp Val Arg Arg			
90	95	100	
gtg ctg ctg cag gcc ttc gat gtg gtg gag agg agc ttc ctg gag tcc	389		
Val Leu Leu Gln Ala Phe Asp Val Val Glu Arg Ser Phe Leu Glu Ser			
105	110	115	120
att gac gac gcc ttg gct gag aag gca agc ctc cag tcg caa ttg cca	437		
Ile Asp Asp Ala Leu Ala Glu Lys Ala Ser Leu Gln Ser Gln Leu Pro			
125	130	135	
gag gga gtc cct cag cac cag ctg cct cct cag tat cag aag atc ctt	485		
Glu Gly Val Pro Gln His Gln Leu Pro Pro Gln Tyr Gln Lys Ile Leu			
140	145	150	
gag aga ctc aag acg tta gag agg gaa att tcg gga ggg gcc atg gcc	533		
Glu Arg Leu Lys Thr Leu Glu Arg Glu Ile Ser Gly Gly Ala Met Ala			
155	160	165	
gtt gtg gcg gtc ctt ctc aac aac aag ctc tac gtc gcc aat gtc ggt	581		
Val Val Ala Val Leu Leu Asn Asn Lys Leu Tyr Val Ala Asn Val Gly			
170	175	180	
aca aac cgt gca ctt tta tgc aaa tcg aca gtg gat ggg ttg cag gtg	629		

Thr Asn Arg Ala Leu Leu Cys Lys Ser Thr Val Asp Gly Leu Gln Val				
185	190	195	200	
				677
aca cag ctg aac gtg gac cac acc aca gag aac gag gat gag ctc ttc				
Thr Gln Leu Asn Val Asp His Thr Thr Glu Asn Glu Asp Glu Leu Phe				
205	210	215		
				725
cgt ctt tcg cag ctg ggc ttg gat gct gga aag atc aag cag gtg ggg				
Arg Leu Ser Gln Leu Gly Leu Asp Ala Gly Lys Ile Lys Gln Val Gly				
220	225	230		
				773
atc atc tgt ggg cag gag agc acc cgg cgg atc ggg gat tac aag gtt				
Ile Ile Cys Gly Gln Glu Ser Thr Arg Arg Ile Gly Asp Tyr Lys Val				
235	240	245		
				821
aaa tat ggc tac acg gac att gac ctt ctc agc gct gcc aag tcc aaa				
Lys Tyr Gly Tyr Thr Asp Ile Asp Leu Leu Ser Ala Ala Lys Ser Lys				
250	255	260		
				869
cca atc atc gca gag cca gaa atc cat ggg gca cag ccg ctg gat ggg				
Pro Ile Ile Ala Glu Pro Glu Ile His Gly Ala Gln Pro Leu Asp Gly				
265	270	275	280	
				917
gtg acg ggc ttc ttg gtg ctg atg tcg gag ggg ttg tac aag gcc cta				
Val Thr Gly Phe Leu Val Leu Met Ser Glu Gly Leu Tyr Lys Ala Leu				
285	290	295		

gag gca gcc cat ggg cct ggg cag gcc aac cag gag att gct gcg atg 965  
 Glu Ala Ala His Gly Pro Gly Gln Ala Asn Gln Glu Ile Ala Ala Met  
 300 305 310

att gac act gag ttt gcc aag cag acc tcc ctg gac gca gtg gcc cag 1013  
 Ile Asp Thr Glu Phe Ala Lys Gln Thr Ser Leu Asp Ala Val Ala Gln  
 315 320 325

gcc gtc gtg gac cgg gtg aag cgc atc cac agc gac acc ttc gcc agt 1061  
 Ala Val Val Asp Arg Val Lys Arg Ile His Ser Asp Thr Phe Ala Ser  
 330 335 340

ggt ggg gag cgt gcc agg ttc tgc ccc cgg cac gag gac atg acc ctg 1109  
 Gly Gly Glu Arg Ala Arg Phe Cys Pro Arg His Glu Asp Met Thr Leu  
 345 350 355 360

cta gtg agg aac ttt ggc tac ccg ctg ggc gaa atg agc cag ccc aca 1157  
 Leu Val Arg Asn Phe Gly Tyr Pro Leu Gly Glu Met Ser Gln Pro Thr  
 365 370 375

ccg agc cca gcc cca gct gca gga gga cga gtg tac cct gtg tct gtg 1205  
 Pro Ser Pro Ala Pro Ala Ala Gly Gly Arg Val Tyr Pro Val Ser Val  
 380 385 390

cca tac tcc agc gcc cag agc acc agc aag acc agc gtg acc ctc tcc 1253

Pro Tyr Ser Ser Ala Gln Ser Thr Ser Lys Thr Ser Val Thr Leu Ser

395

400

405

ctt gtc atg ccc tcc cag ggc cag atg gtc aac ggg gct cac agt gct 1301

Leu Val Met Pro Ser Gln Gly Gln Met Val Asn Gly Ala His Ser Ala

410

415

420

tcc acc ctg gac gaa gcc acc ccc acc ctc acc aac caa agc ccg acc 1349

Ser Thr Leu Asp Glu Ala Thr Pro Thr Leu Thr Asn Gln Ser Pro Thr

425

430

435

440

tta acc ctg cag tcc acc aac acg cac acg cag acg agc agc tcc agc 1397

Leu Thr Leu Gln Ser Thr Asn Thr His Thr Gln Ser Ser Ser Ser

445

450

455

tct gac gga ggc ctc ttc cgc tcc cgg ccc gcc cac tcg ctc ccg cct 1445

Ser Asp Gly Gly Leu Phe Arg Ser Arg Pro Ala His Ser Leu Pro Pro

460

465

470

ggc gag gac ggt cgt gtt gag ccc tat gtg gac ttt gct gag ttt tac 1493

Gly Glu Asp Gly Arg Val Glu Pro Tyr Val Asp Phe Ala Glu Phe Tyr

475

480

485

cgc ctc tgg agc gtg gac cat ggc gag cag agc gtg gtg aca gca ccg 1541

Arg Leu Trp Ser Val Asp His Gly Glu Gln Ser Val Val Thr Ala Pro

490

495

500

tagggcagcc ggaggaatg 1560

<210> 4

<211> 504

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Ala Gln Arg Arg Ser Leu Leu Gln Ser Glu Gln Gln Pro Ser

5	10	15
---	----	----

Trp Thr Asp Asp Leu Pro Leu Cys His Leu Ser Gly Val Gly Ser Ala

20	25	30
----	----	----

Ser Asn Arg Ser Tyr Ser Ala Asp Gly Lys Gly Thr Glu Ser His Pro

35	40	45
----	----	----

Pro Glu Asp Ser Trp Leu Lys Phe Arg Ser Glu Asn Asn Cys Phe Leu

50	55	60
----	----	----

Tyr Gly Val Phe Asn Gly Tyr Asp Gly Asn Arg Val Thr Asn Phe Val

65	70	75	80
----	----	----	----

Ala Gln Arg Leu Ser Ala Glu Leu Leu Leu Gly Gln Leu Asn Ala Glu

85 90 95

His Ala Glu Ala Asp Val Arg Arg Val Leu Leu Gln Ala Phe Asp Val

100 105 110

Val Glu Arg Ser Phe Leu Glu Ser Ile Asp Asp Ala Leu Ala Glu Lys

115 120 125

Ala Ser Leu Gln Ser Gln Leu Pro Glu Gly Val Pro Gln His Gln Leu

130 135 140

Pro Pro Gln Tyr Gln Lys Ile Leu Glu Arg Leu Lys Thr Leu Glu Arg

145 150 155 160

Glu Ile Ser Gly Gly Ala Met Ala Val Val Ala Val Leu Leu Asn Asn

165 170 175

Lys Leu Tyr Val Ala Asn Val Gly Thr Asn Arg Ala Leu Leu Cys Lys

180 185 190

Ser Thr Val Asp Gly Leu Gln Val Thr Gln Leu Asn Val Asp His Thr

195 200 205

Thr Glu Asn Glu Asp Glu Leu Phe Arg Leu Ser Gln Leu Gly Leu Asp

210 215 220

Ala Gly Lys Ile Lys Gln Val Gly Ile Ile Cys Gly Gln Glu Ser Thr

225

230

235

240

Arg Arg Ile Gly Asp Tyr Lys Val Lys Tyr Gly Tyr Thr Asp Ile Asp

245

250

255

Leu Leu Ser Ala Ala Lys Ser Lys Pro Ile Ile Ala Glu Pro Glu Ile

260

265

270

His Gly Ala Gln Pro Leu Asp Gly Val Thr Gly Phe Leu Val Leu Met

275

280

285

Ser Glu Gly Leu Tyr Lys Ala Leu Glu Ala Ala His Gly Pro Gly Gln

290

295

300

Ala Asn Gln Glu Ile Ala Ala Met Ile Asp Thr Glu Phe Ala Lys Gln

305

310

315

320

Thr Ser Leu Asp Ala Val Ala Gln Ala Val Val Asp Arg Val Lys Arg

325

330

335

Ile His Ser Asp Thr Phe Ala Ser Gly Gly Glu Arg Ala Arg Phe Cys

340

345

350

Pro Arg His Glu Asp Met Thr Leu Leu Val Arg Asn Phe Gly Tyr Pro

355                    360                    365

Leu Gly Glu Met Ser Gln Pro Thr Pro Ser Pro Ala Pro Ala Ala Gly

370                    375                    380

Gly Arg Val Tyr Pro Val Ser Val Pro Tyr Ser Ser Ala Gln Ser Thr

385                    390                    395                    400

Ser Lys Thr Ser Val Thr Leu Ser Leu Val Met Pro Ser Gln Gly Gln

405                    410                    415

Met Val Asn Gly Ala His Ser Ala Ser Thr Leu Asp Glu Ala Thr Pro

420                    425                    430

Thr Leu Thr Asn Gln Ser Pro Thr Leu Thr Leu Gln Ser Thr Asn Thr

435                    440                    445

His Thr Gln Ser Ser Ser Ser Ser Asp Gly Gly Leu Phe Arg Ser

450                    455                    460

Arg Pro Ala His Ser Leu Pro Pro Gly Glu Asp Gly Arg Val Glu Pro

465                    470                    475                    480

Tyr Val Asp Phe Ala Glu Phe Tyr Arg Leu Trp Ser Val Asp His Gly

485                    490                    495

Glu Gln Ser Val Val Thr Ala Pro

500

<210> 5

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence

<400> 5

ccggaattcc accatggagc ttccggcagtt atcc

34

<210> 6

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence

<400> 6

ccggaattcc tactgacaag gatactgt

28

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence

<400> 7

gtacttcagc acagtttag agaac

25

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence

<400> 8

ggttgcattgc tgtgaaga

18

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence

<400> 9

cggaaattcga gctccggcag tgtcgcg

27

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence

<400> 10

aactgcaggc tactgacaag gatactgtaa

30